line 22, after "AGT AG" insert --(SEQ ID NO:53)--;

line 23, after ". . . . ." insert --(SEQ ID NO:68)--;

line 25, after "CCC AT" inset --(SEQ ID NO:54)--;

line 27, after "GTG G" insert --(SEQ ID NO:55)--;

line 29, after "TGA A" insert --(SEQ ID NO:56)--; and

line 31, after "CTG G" insert --(SEQ ID NO:57)--.

Page 10, line 1, after "GGA" insert --(SEQ ID NO:58)--;

line 3, after "TCT TTT" insert --(SEQ ID NO:59)--;

line 6, after "TCC C" insert --(SEQ ID NO:60)--;

line 10, after "GTT GAT" insert --(SEQ ID NO:61)--;

line 12, after "CTG TA" insert --(SEQ ID NO:62)--;

line 14, after "TCT GC" insert --(SEQ ID NO:63)--;

line 16, after "CTC TA" insert --(SEQ ID NO:64)--;

line 20, after "ACC T" insert --(SEQ ID NO:65)--;

line 22, after "TGA GAG" insert --(SEQ ID NO:66)--; and

line 24, after "CCA AA" insert --(SEQ ID NO:67)--.

After page 28 insert the attached Sequence Listing pages.

IN THE CLAIMS:

Please cancel claims 1-26.

Please add the following new claims.

--27. A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

Subc1

Cont

a'

a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of;

nucleotides 6905-6930, 7055-7077, 7360-7384, 7832-7857, 8844-8869, 7629-7647, and 8224-8242 of the *env* gene of HIV-1 Bru;

nucleotides 6930-6905, 7384-7360, 7857-7832, 8869-8844, and nucleotides 8242-8224 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928, 7053-7075, 7349-7373, 7821-7846, 7612-7630, 8213-8231, and 8836-8861 of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903, 7373-7349, 7846-7821, 8861-8836, and 8231-8213 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885, 7010-7032, 7306-7330, 7775-7800, 8787-8812, 7572-7590, and 8167-8185 of the *env* gene of HIV-1 Eli; and

nucleotides 6885-6860, 7330-7306, 7800-7775, 8812-8787, and 8185-8167 of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

28. A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);

MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);

MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);

MMy7: ATC CTC A0G AGG GGA CCC AGA AAT T (SEQ ID NO:49);

MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);

MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);

MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

LAW OFFICES
FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56); and

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57);

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

29. An antibody capable of binding to the polypeptide of claims 27 or 28.

30. A method for the *in vitro* diagnosis of the infection of a mammal by a virus of the HIV-1, HIV-2, or SIV type, said virus comprising at least one polypeptide antigen, said method comprising placing a biological sample taken from said mammal in contact with antibody according to claim 29, and detecting the immunological complex formed between said antigen and said antibody.

31. A kit for the diagnosis of infection of a mammal by a virus of the HIV-1, HIV-2, or SIV type, said kit comprising an antibody according to claim 29 and reagents for the detection of the immunological complex formed between said antibody and said antigen.

32. A composition comprising at least one polypeptide according to claim 27 in combination with a pharmaceutically acceptable vehicle.

33. A composition comprising at least one polypeptide according to claim 28 in combination with a pharmaceutically acceptable vehicle.--

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000